

Figure 1

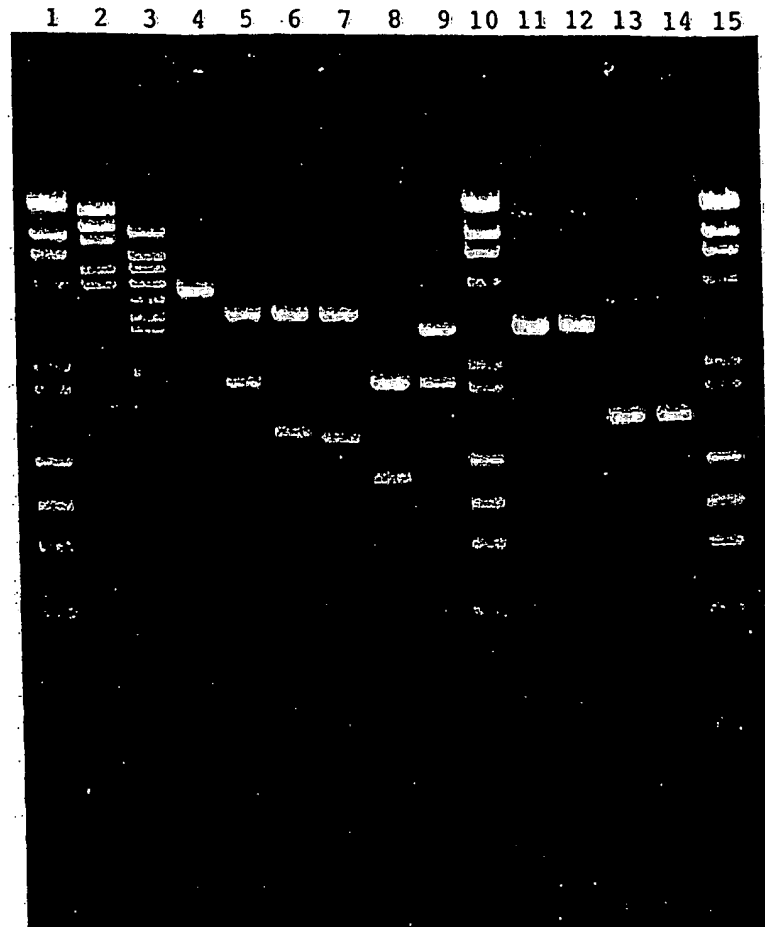


Figure 2

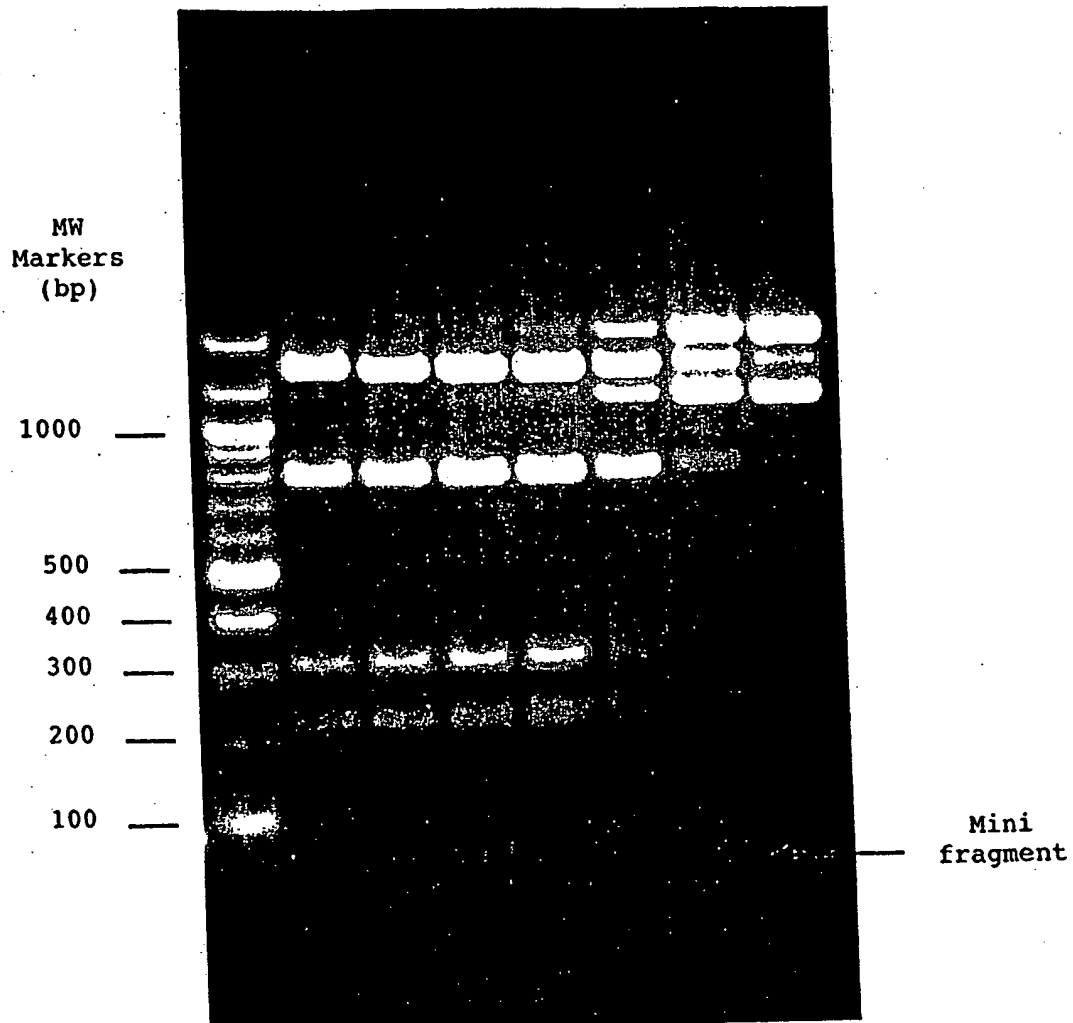


Figure 3

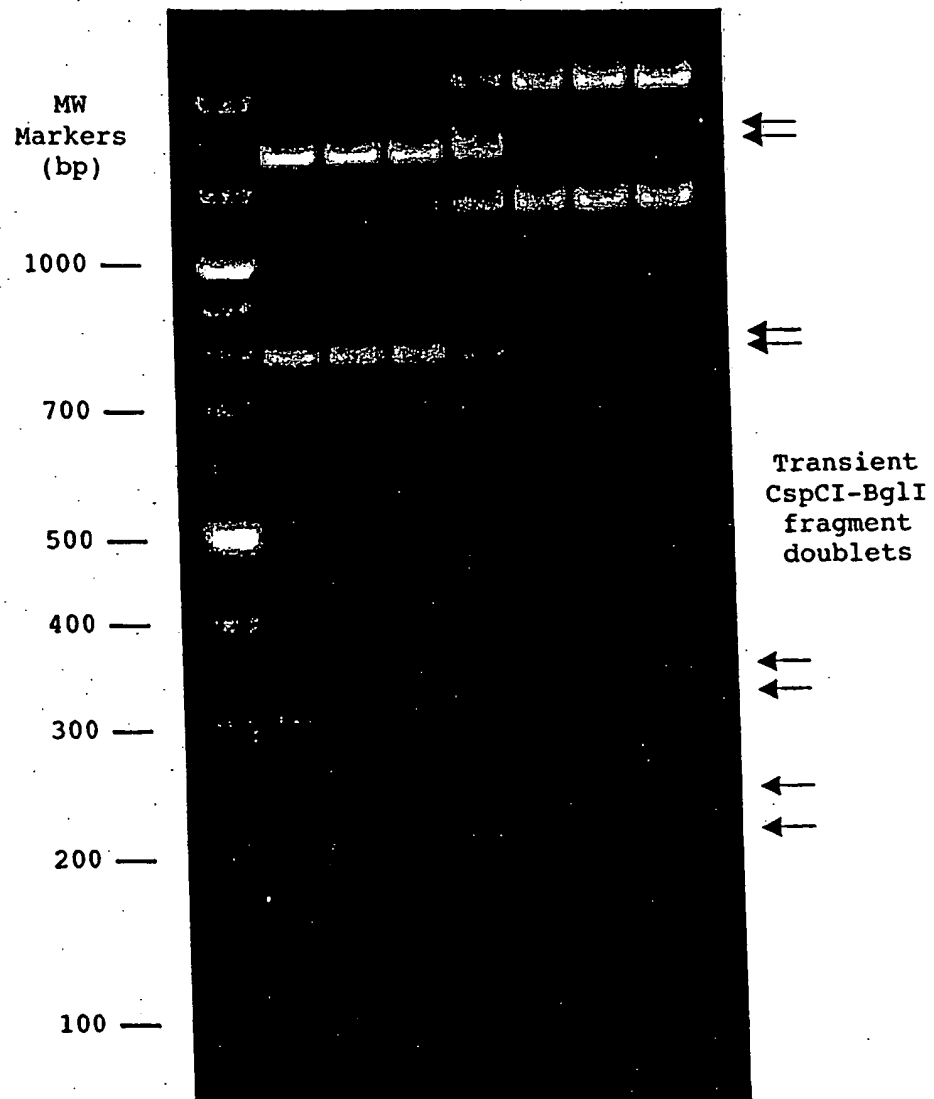


Figure 4a

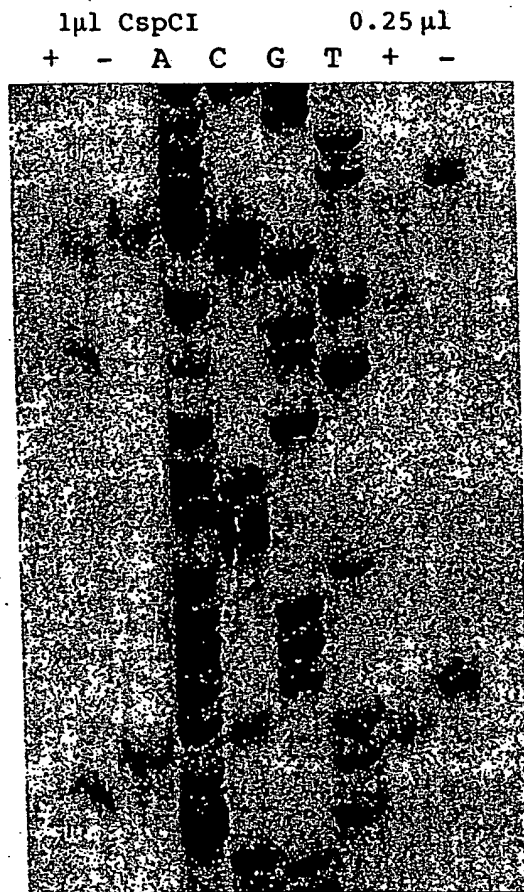


Figure 4b

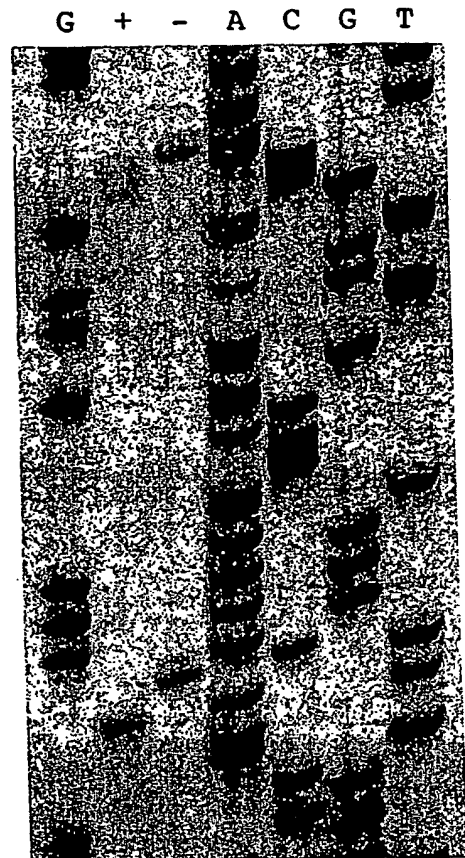


Figure 5a. pCsp-4, fwd primer (SEQ ID NO:1)

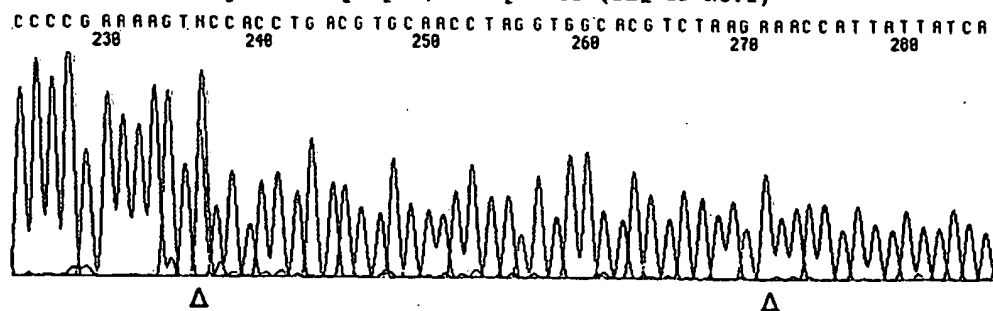


Figure 5b. pCsp-4, rev primer (SEQ ID NO:2)

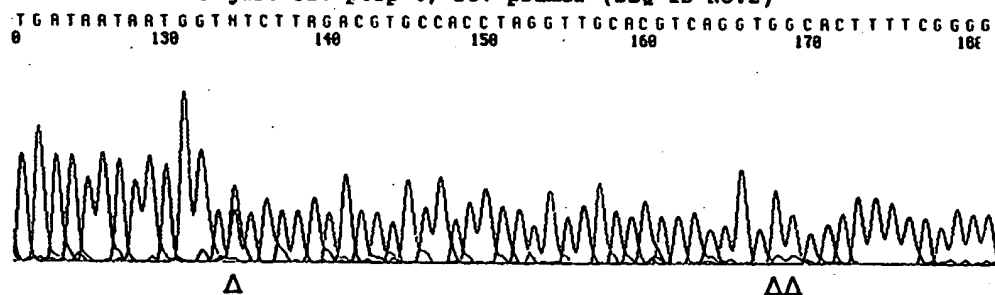


Figure 5c. pCsp-1, fwd primer (SEQ ID NO:3)

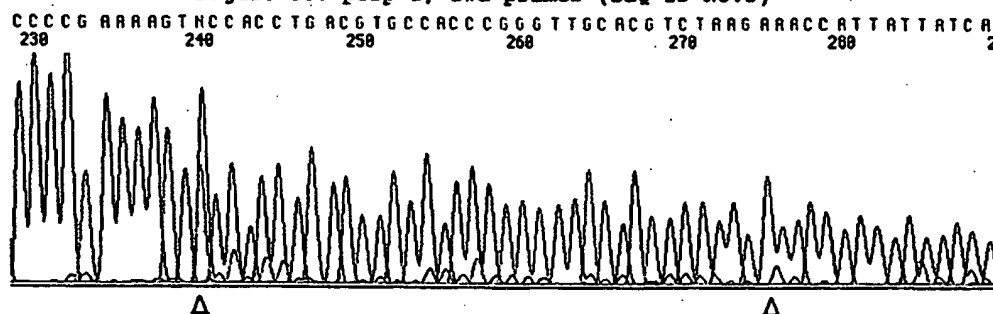


Figure 5d. pCsp-1, rev primer (SEQ ID NO:4)

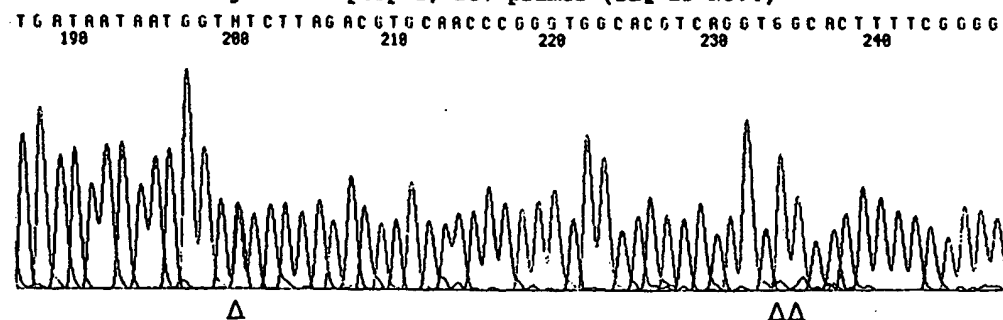


Figure 6-2

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2201 CTGCTGGTGA GTGGGACCTT GATTGCGTTG ATGAACAACA CATTTCATCAA
2251 GACCTTTGAC GCTCTACCTG CAGAAGATGT GCAGGAAGCG TGGCTGACGG
2301 CTATCAAGAA GGAGCTGGAC AAAGCTTCTA TCCCCAGGC CAAGAAGGAC
2351 ACGATGCTGC AGCCGTATAC GACGATTGCG GTTAATCCCA ATCTTGGCAA
2401 GCCTGACAGC AAGACGGCTA AAGAGTATCC AGATGGAGTT TTCAAGGAAA
2451 TAATCACCCG CATCGCCGAC AACGTCTGGC CCTACATCAA TGCTTTTCAC
2501 GACTTTGATG TGGTCGGACA ATTCTACGGT GAGTTTCTGA AATATACTGC
2551 GGGCGACAAA AAAGCGCTGG GCATCGTGCT GACGCCGCGC CATGTGGCTG
2601 AACTGTTCTC GCTCATCGCC AACGTTAACC CCAAGTCTAA GGTGCTGGAC
2651 ATCTGTGCGG GCACGGGCGG CTTTCTCATC TCGGCCATGC AACACATGCT
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2801 ATGATTCTGC GTGGTGATGG TAAGGCTAAC CTGCACCAGG CCAGTTGCTT
2851 TGATAATGCA GTGATTGCGG CCGTGACAGAA GATGAAGCCC AACGTGGGCA
2901 TGCTTAACCC CCCGTATTCTG CAGTCCAAGA GCGACGCGGA ACTGCATGAG
2951 CTGTATTTCTG TCAAGCAAAT GCTCGACACG CTTACACCAG GTGGAGTTGG
3001 TATCGCGATT GTTCCCATGT CAAGCGCCAT CTCGCCAAC CCAATGCGTG
3051 AAGAGCTGAT GAAGTACCAC TCACTGGATG CGGTCATGTC AATGCCCCAG
3101 GAGCTGTTTT ATCCAGTGGG CACGGTCACC TGTGTCATGG TCTGGATTGC
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3501 AACGACCTTT TTCATCTGGA GTACGGTCAC AGCCTGGAGT TGAACCGGCT
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3651 GCAGCCGCAG GCACCATCAG CGTAGCGCTG GGAGGGCAAG GTGGCGCAGG
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3901 GGGTGACATC AGCGAACCCC GATGCCTACC AAGGTGTCAG GTCCCCCGCA
3951 AGTGTTTCATC CAGTCGGCAC GCTGGCTGTG AGCAACTGGA AGGCTTTCAT
4001 TCTTCAAGAC TTGTTTACCA TCCGTAAAGG ACAGCGACTC ACCAAGGCCA
4051 ACATGTTGCC CGGTACGGTG CCCTACATCG GCGCATCGGA CACTTCCAAC
4101 GGCCTTACTG CGCACATCGG GCAAAAACCA ATCCACGAGG CCGGCACCAT
4151 CAGCGTCACA TATGACGGTT CAATAGCTGA AGCGTTTAC GACCCCTCCC
4201 CATTTTGGGC ATCGGATGCT GTGAACGTGC TCTATCCCAA GGGTTTCACA
4251 CTCACACCGG CCACTGCCTT GTTTATCTGC GCAATCATCA GGATGGAGAA
4301 ATATCGCTTC AACTATGGCC GAAAATGGCA CTTAGAGCGT ATGCGAGAGA
4351 CAGTTATCAG GTTACCAGCT ACTGCAACAG GTGCACCAGA TTGGGACTTT
4401 ATGGAGAAAT ACATCAAAAC TTTGCCCTAT AGCTCGCAGT TGCAATAATC

Figure 6-3

4451 ATGGCTGATT TCCTAAATTT CCTGCCGCAT CTACGGGTAT TGCATGTTCA
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4551 CCGCTTGCCC GGCCTGCGGT GAAAAGCCTT CCCATTCAGG GAAGGCTTTA
4601 ATCGAGTTAT AGATCT

Figure 7a (SEQ ID NO:6)

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1 ATGGCGAACG AACGCAAAAC AGAATCCTTA GTTCGAGACC AGCTACGGAC
51 ATTTGGCTAC TACGAACCGG ACAACGGCAT TTCTGTAGAG GAGCAAAAGT
101 CCGAGATTGT CAAGATTAAG GGTTCGCTTT CAAAAGCAAG TAAGAACGCC
151 AAGGGCAATA TTGGTTATCC CGAGTTCATC ATCTCTAACC GGAAAGATAC
201 TGCATTCTCTG ATAGTTGTGG AGTGCAAGCC GGATGTGAAA AAGCACGAGA
251 GCCCAAGCCG TGATAAGCCG GTAGACTATG CCGTGGATGG CGTTCTCCAC
301 TACGCCAGAC ACCTAGCCAA GCACATAACC GTATTGGCGG TGGCTGTGAG
351 CGGCACGACG GCAAGTTCTA TGAAGGTGTC CAACTTCCTT GTGCCTGCGG
401 GTACCACGGA TGTGAAGGCG CTGGTCAACG AGAGTAATTC CTCAGTTGCC
451 GAATTGGTGC CTTATGATGA CTACTACCGC CTGGCGTCTT ATGATCCGGA
501 TGTTCGCTCAG AAGCGCCACT CTGACTTGCT GGCCTTCTCA CGCGAGCTGC
551 ACGAGTTTAT TTGGACGAAG GCAAAAATCT CCGAAGAAGA AAAGCCTCTG
601 CTGGTGAGTG GGACCTTGAT TGCCTTGATG AACAACACAT TCATCAAGAC
651 CTTTGACGCT CTACCTGCAG AAGATGTGCA GGAAGCGTGG CTGACGGCTA
701 TCAAGAAGGA GCTGGACAAA GCTTCTATCC CCCAGGCCAA GAAGGACACG
751 ATGCTGCAGC CGTATACGAC GATTGCGGTT AATCCCAATC TTGGCAAGCC
801 TGACAGCAAG ACGGCTAAAG AGTATCCAGA TGGAGTTTTT AAGGAAATAA
851 TCACCCGCAT CGCCGACAAC GTCTGGCCCT ACATCAATGT CTTTCACGAC
901 TTTGATGTGG TCGGACAATT CTACGGTGAG TTTCTGAAAT ATACTGCGGG
951 CGACAAAAAA GCGCTGGGCA TCGTGCTGAC GCCGCGCCAT GTGGCTGAAC
1001 TGTTCGCGCT CATCGCCAAC GTTAACCCCA AGTCTAAGGT GCTGGACATC
1051 TGTGCGGGCA CGGGCGGCTT TCTCATCTCG GCCATGCAA ACATGCTCAA
1101 GAAGGCCGTA ACGGACAAAG AGCGCAACGA CATCAAGCAA AATCGGCTCA
1151 TCGGGATTGA AAACAACCCC AAGATGTTTG CCTTGGCTGC CAGCAACATG
1201 ATTCTGCGTG GTGATGGTAA GGCTAACCTG CACCAGGCCA GTTGCTTTGA
1251 TAATGCAGTG ATTGCGGCCG TGCAGAAAGT GAAGCCCAAC GTGGGCATGC
1301 TTAACCCCCC GTATTGCGAG TCCAAGAGCG ACGCGGAAC TGCATGAGCTG
1351 TATTTGCTCA AGCAAATGCT CGACACGCTT ACACCAGGTG GAGTTGGTAT
1401 CGCGATTGTT CCCATGTCAA GCGCCATCTC GCCCAACCCA ATGCGTGAAG
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1501 CTGTTTTATC CAGTGGGCAC GGTACCTGT GTCATGGTCT GGATTGCCGG
1551 TGTGCCACAT GAGCAAATGT CCAAGAAGAC ATGGTTTGGC TACTGGCGCG
1601 ACGATGGCTT TGTGAAAACC AAGCATAAGG GCGCATCGA CATGAATGGC
1651 ACCTGGCCAG ACATCCGTGA CCGATGGATT GAAATGTATC GCAATCGCGA
1701 AGTGCATGCT GCGGAGAGCA TCATGCAGAA GGTAGGCCCC GATGATGAAT
1751 GGTGCGCTGA AGCCTATATG GAAACGGACT ACTCAGTGCT GACTCAGTCC
1801 GACTTTGAGA AGGTCGTTCA AAGCTACGCG CTATTTAAAC TATTTGGTCA
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Figure 7b (SEQ ID NO:6)

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51 GTTGAACCGG CTAGAGCAAT CCACAGCAGC CGATGCCGTC AACTTCGTTG
101 GACGGGCAGC TAGGAACAAT GGAGTCACCG CACGCGTGGC TCCCCCTCCA
151 AACTTGAAAC CGGCAGCCGC AGGCACCATC AGCGTAGCGC TGGGAGGGCA
201 AGGTGGCGCA GGAGTCGCCT TCCTCCAACC GCGTCCCTAC TTTTGTGGCC
251 GCGATGTGAT GGTGCTGACC CCCAAGAAGC ACATGACAGA CCAAGAAAAG
301 CTGTGGTGGG TCATGTGCAT CACAGCCAAC CGTTTCCGCT TTGGATTGG
351 TCGCCAAGCT AATCGGACGC TAAAGGACTT GAATCTGCCT GCGCCCCAAA
401 AAACCTCAAG CTGGGTGCAT ACAGCGAACC CCGATGCCTA CCAAGGTGTC
451 AGGTCCCCCG CAAGTGTTCA TCCAGTCGGC ACGCTGGCTG TGAGCAACTG
501 GAAGGCTTTC ATTCTTCAAG ACTTGTTTAC CATCCGTAAA GGACAGCGAC
551 TCACCAAGGC CAACATGTTG CCCGGTACGG TGCCCTACAT CGGCGCATCG
601 GACACTTCCA ACGGCGTTAC TGCGCACATC GGGCAAAAAC CAATCCACGA
651 GGGCGGCACC ATCAGCGTCA CATATGACGG TTCAATAGCT GAAGCGTTTT
701 ACCAGCCCTC CCCATTTTGG GCATCGGATG CTGTGAACGT GCTCTATCCC
751 AAGGGTTTCA CACTCACACC GGCCACTGCC TTGTTTATCT GCGCAATCAT
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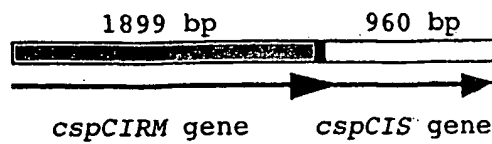


Figure 8a

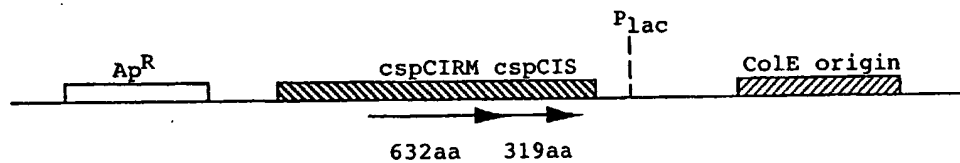


Figure 8b

Figure 9a (SEQ ID NO:8)

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51 KGNIGYPEFI ISNRKDTAFL IVVECKPDVK KHESPSRDKP VDYAVDGV LH
101 YARHLAKHYT VLAVAVSGTT ASSMKVSNFL VPAGTTDVKA LVNESNSSVA
151 ELVPYDDYR LASYDPDVAQ KRHSDLLAFS RELHEFIWTK AKISEEEKPL
201 LVSGTLIALM NNTFIKTFDA LPAEDVQEAW LTAIKKELDK ASIPQAKKDT
251 MLQPYTTIAV NPNLGKPSDK TAKEYPDGVF KEIITRIADN WVPYINV FHD
301 FDVVGQFYGE FLKYTAGDKK ALGIVLTPRH VAELFSLIAN VNP KSKVLDI
351 CAGTGGFLIS AMQHMLKKAV TDKERN DIKQ NRLIGIENNP KMFALAASNM
401 ILRGDGKANL HQASCFDNAV IAAVQKMKPN VGMLNPPYSQ SKSDAELHEL
451 YFVKQMLDTL TPGGVGIAIV PMSSAISPNP MREELMKYHS L DAVMSMPQE
501 LFYPVGTVTC VMWVIAGVPH EQMSKKTWFG YWRDDGFVKT KHKGRIDMNG
551 TWPDIRDRWI EMYRNREVHA GESIMQKVG P DDEWCAEAYM ETDYSVLTQS
601 DFEKVVSQSYA LFKLFGQGSS QSEVKGATDA ED

Figure 9b (SEQ ID NO:9)

1 MPKINDLFHL EYGHSLLELR LEQSTAADAV NFVGRAARNN GVTARVAPPP
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101 LWWVMCITAN RFRFGFGRQA NRTLKDLNLP APQKTPSWVH TANPDAYQGV
151 RSPASVHPVG TLAVSNWKAF ILQDLFTIRK GQRLTKANML PGTVPYIGAS
201 DTSNGVTAHI GQKPIHEGGT ISVTYDGSIA EAFYQPSPFW ASDAVNVLYP
251 KGFTLTPATA LFICAIIRME KYRFNYGRKW HLERMRETVI RLPATATGAP
301 DWDFMEKYIK TLPYSSQLQ